

RAW SEQUENCE LISTING DATE: 10/04/2001
 PATENT APPLICATION: US/09/887,038 TIME: 08:07:45

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5 <110> APPLICANT: Kaplan, Aaron
 7 Lieman-Hurwitz, Judy
 9 Schatz, Daniella
 11 Mittler, Ron
 13 Ronen-Tarazi, Michal
 15 Bonfil, David J.
 19 <120> TITLE OF INVENTION: ENHANCING INORGANIC CARBON FIXATION BY PHOTOSYNTHETIC ORGANISMS

23 <130> FILE REFERENCE: 01/22171

C--> 27 <140> CURRENT APPLICATION NUMBER: US/09/887,038

C--> 27 <141> CURRENT FILING DATE: 2001-09-17

27 <160> NUMBER OF SEQ ID NOS: 9

31 <170> SOFTWARE: PatentIn version 3.1

35 <210> SEQ ID NO: 1

37 <211> LENGTH: 4957

39 <212> TYPE: DNA

41 <213> ORGANISM: Synechococcus sp.

45 <400> SEQUENCE: 1

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52	tgtttttca	agaccgacag	gtcgatggcg	tgattttggct	agccctcagt	ggcaatgtcc	240
54	agctgcaggc	gatcggtggct	cagggtgtc	gtccagttgg	ccgcgtttgg	catgtggcag	300
56	cggcggagcg	caacattctg	cggcaacttc	agaccaaga	cgaggaaccg	atcgccgcgc	360
58	tgcaagccct	acagtcagtc	ctgcgtgatc	tctccctga	attacagcga	tcgctctgtg	420
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62	acctgtgtgg	gtttgatccc	cgcactgggt	ctgttagcaat	ccgcgatcgc	atcgagttg	540
64	ggcagcggct	gcagctgcac	gtacgggatg	cccagacagc	ggcggatgac	ctcgagcggc	600
66	aactggggca	atggtgcgg	cagcatgcga	caaaaaccagc	agcttccctc	ttgtttccct	660
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72	ctggcagcac	ctacctgcat	ggctacacat	cggtgtggc	tttgctgtcg	gccaaaactc	840
74	actagcgcca	gcgagacctg	attgtcgatc	tgctgagcgc	gactgttagcg	ctggaaatag	900
76	gccccggacct	gagcaggcgc	atcgcccaag	ctgaccgtag	tatcaccgtc	agccacccccc	960
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82	aaaaacgtttt	taaatcagtc	ttgatccgg	agcgatcgca	cccgacggga	ctctagttct	1140
84	agttgccaac	tttcagcggc	aggttgtacg	gttcccgatc	gttagggatg	gggatagctg	1200
86	accaaggaac	cggtcgtgac	ttcccagaga	gcacccgt	gactgggtggc	ttggatgtgg	1260
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92	aacacattgt	ggtgaatcat	cacccagcgt	tggctagcgg	tggaaagtggc	gagttcttgt	1440
94	tgcagccagt	tgagttgcgc	gcaatcgact	cgcccccgat	gcatgtatg	gcccgcgtca	1500
96	tcaaaaagcga	tcgaattcag	cgcaaacaga	tcgagatccg	gtgcgatcgt	gcagcgatag	1560
98	taggggcgt	cgctcgtaa	gccaaggatct	tgatagagct	cgacaaactc	ggccacaccg	1620
100	gtgcgatcgc	gatcgctcgc	tgcggcgggc	atatcggt	tgcggcgcac	cacatagacc	1680
102	ggataggcga	actggcgaa	ttgttgcgc	agccactgtat	ggttttcccg	ctccccgtgc	1740
104	tgggttaaat	ccccggcag	caacaggaag	tccaaatcca	gcgcgtccag	ttctgtcagg	1800

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106	atttgctcaa aagccgaaat gctgcactca atcaaataatggaa	1860
108	attgtctgcg gcagtccaaat gtggagatcg ctcacgcgcg	1920
110	attgccatcc cctcagctat cgagcccgat tcttagggcga	1980
112	tccatgtca agcattcatg gccagaggta gcgttgcga	2040
114	agaaattcca agtggtcacg acttggccgg attggcaaca	2100
116	gccccgtcga ttggatatt ggctgtgcgcgcgtt	2160
118	gacaacctga gtgaaattat ctggggctgg aaattcgtga	2220
120	acgcgatcgc cccgcaacgt gaactgacca atctctacta	2280
122	tggacttggaa accgctgcgt cgatcgctgc	2340
124	agttcccgaa tccttgggttc aagaaacgaa atcaaaagcg	2400
126	tggtgcaagc cctcgcgact gcgttacctg ctggtgca	2460
128	tgcttggaaatgtgcgaaac actttgcggc ggaacccccc	2520
130	cctgcttggaa ctggctgcgcg gaaaatccgc tgccgcgtcc	2580
132	ttcaaaacaa acagttgcca gtctaccgtg ctctttcat	2640
134	ctcttaaggc aagcggttgcgcgatcgca tgactgtctg	2700
136	attaccaacc ccaacagtgg ggccacacga gtttcttgc	2760
138	gagcttggcg ggctccacgc cagctgttgg ttttgtctga	2820
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150	tcgtgatcac atcgctttt gtcagtgtct acggcctaa	3180
152	aagagcttggc gacttgggtg gatcgcaact cggttgcga	3240
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156	cagcagcgat cgggggtgtgg cgccgcgtgc tcccaagct	3360
158	gtgcgagcag ctatgtctg atccctacact acagtcgcgg	3420
160	ccatgatttt tgcttggcgtt tatttagggc tctactgtt	3480
162	cctggcgacg ctgcttattc ccagtcgtat tgggtggact	3540
164	cggtgcttgg acttgagccg ttgcgcgtgc gcgtgttag	3600
166	acagcagcaa caacttccgg atcaatgtct ggctggcggt	3660
168	ggccttggct gggcatcgcc cccggcaata cccgcattaa	3720
170	aacaggcgcg cttaacggcg ttgagccct actccgtccc	3780
172	ggggactact gggcttgacg gccttcgtt ggctgtctgt	3840
174	tgcggcaggt gagccgactg cggcgcgtat gcaatcccc	3900
176	gcttggccgg tttggcagga atgctggctc acggctgttt	3960
178	cggaaaggccat tacgtctgg tggctctgtt ttggagccat	4020
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182	cccaacaaat tcctgtgcac ccgactggat ccaccaccta	4140
184	cggtgatct agggtcataa cgaactccga cccgcgtatgc	4200
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188	cagttggctt ggaaggcaggc tgcgagaagc caccgcatac	4320
190	cttccgcaaa gactacgatc gccacggcg ctgtccagc	4380
192	tgtcatagca gtccgcagac aagtttaggac aacttcata	4440
194	cagccgtgt ccgtgggggt gcgcaatcac cccacaccc	4500
196	ccccccaggcc ccccgcaaca agatttccga taagggcat	4560
198	cgggtaaaac tagcccggtgt tagccatggg tttagacta	4620
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202	aaaaatcacg accgcccacg tccgaggct ttgtgttgg	4740

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208	ttccagctgg	gtatTTTta	gtcgatctac	cagtgggtgc	ggccgatgg	tcgcaaccca	4920										
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242	tcgggttgcg	acttcacctc	acgggttac	agctatctgg	gcaaccccaa	cctgctggct	600										
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258	accgcctta	acctggttt	tccctctat	caacaggcgc	gcittacggc	tttgcgcgc	1080										
260	tactccgtcc	cgctggaagt	cgcggttgag	ggcggactac	tgggcttgac	ggccttcgt	1140										
262	tggctgcgtc	tgtcacggc	ggtgacggcg	gtgcggcagg	tgagccgact	gcggcgcgat	1200										
264	cgcaatcccc	aagctttt	gttgcgtgt	agcttggccg	gttggcagg	aatgcgtgg	1260										
266	cacggcttgt	ttgataccgt	gtctatcg	ccggaaagcca	gtacgctctg	gtggcttgt	1320										
268	attggagcga	tcgcgagttt	ctggcagccc	caaccttcca	agcaactccc	tccagaagcc	1380										
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289	Trp	Gly	His	Ser	Ser	Phe	Lle	His	Arg	Lle	Phe	Gly	Ser	Lle	Arg	Ala	
290						20			25					30			
293	Trp	Arg	Ala	Ser	Ser	Gln	Lle	Lle	Val	Trp	Ser	Glu	Ala	Lle	Gly	Gly	
294						35			40			45					
297	Phe	Lle	Lle	Ala	Val	Val	Tyr	Gly	Ser	Ala	Pro	Phe	Val	Pro	Ser	Ser	
298						50			55			60					
301	Ala	Lle	Gly	Lle	Gly	Lle	Ala	Ala	Ile	Ala	Ala	Tyr	Trp	Ala	Lle	Lle	
302	65					70				75				80			
305	Ser	Lle	Thr	Asp	Ile	Asp	Lle	Arg	Gln	Ala	Thr	Pro	Ile	His	Trp	Lle	

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306	85	90	95
309	Val Leu Leu Tyr Trp Gly Val Asp Ala Leu Ala Thr Gly Leu Ser Pro		
310	100	105	110
313	Val Arg Ala Ala Ala Leu Val Gly Leu Ala Lys Leu Thr Leu Tyr Leu		
314	115	120	125
317	Leu Val Phe Ala Leu Ala Ala Arg Val Leu Arg Asn Pro Arg Leu Arg		
318	130	135	140
321	Ser Leu Leu Phe Ser Val Val Val Ile Thr Ser Leu Phe Val Ser Val		
322	145	150	155
325	Tyr Gly Leu Asn Gln Trp Ile Tyr Gly Val Glu Glu Leu Ala Thr Trp		
326	165	170	175
329	Val Asp Arg Asn Ser Val Ala Asp Phe Thr Ser Arg Val Tyr Ser Tyr		
330	180	185	190
333	Leu Gly Asn Pro Asn Leu Leu Ala Ala Tyr Leu Val Pro Thr Thr Ala		
334	195	200	205
337	Phe Ser Ala Ala Ala Ile Gly Val Trp Arg Gly Trp Leu Pro Lys Leu		
338	210	215	220
341	Leu Ala Ile Ala Ala Thr Gly Ala Ser Ser Leu Cys Leu Ile Leu Thr		
342	225	230	235
345	Tyr Ser Arg Gly Gly Trp Leu Gly Phe Val Ala Met Ile Phe Val Trp		
346	245	250	255
349	Ala Leu Leu Gly Leu Tyr Trp Phe Gln Pro Arg Leu Pro Ala Pro Trp		
350	260	265	270
353	Arg Arg Trp Leu Phe Pro Val Val Leu Gly Gly Leu Val Ala Val Leu		
354	275	280	285
357	Leu Val Ala Val Leu Gly Leu Glu Pro Leu Arg Val Arg Val Leu Ser		
358	290	295	300
361	Ile Phe Val Gly Arg Glu Asp Ser Ser Asn Asn Phe Arg Ile Asn Val		
362	305	310	315
365	Trp Leu Ala Val Leu Gln Met Ile Gln Asp Arg Pro Trp Leu Gly Ile		
366	325	330	335
369	Gly Pro Gly Asn Thr Ala Phe Asn Leu Val Tyr Pro Leu Tyr Gln Gln		
370	340	345	350
373	Ala Arg Phe Thr Ala Leu Ser Ala Tyr Ser Val Pro Leu Glu Val Ala		
374	355	360	365
377	Val Glu Gly Gly Leu Leu Gly Leu Thr Ala Phe Ala Trp Leu Leu Leu		
378	370	375	380
381	Val Thr Ala Val Thr Ala Val Arg Gln Val Ser Arg Leu Arg Arg Asp		
382	385	390	395
385	400		
386	Arg Asn Pro Gln Ala Phe Trp Leu Met Ala Ser Leu Ala Gly Leu Ala		
389	405	410	415
389	Gly Met Leu Gly His Gly Leu Phe Asp Thr Val Leu Tyr Arg Pro Glu		
390	420	425	430
393	445		
394	Ala Ser Thr Leu Trp Trp Leu Cys Ile Gly Ala Ile Ala Ser Phe Trp		
397	435	440	
398	Gln Pro Gln Pro Ser Lys Gln Leu Pro Pro Glu Ala Glu His Ser Asp		
401	450	455	460
402	Glu Lys Met		

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 407 <211> LENGTH: 1425
 409 <212> TYPE: DNA
 411 <213> ORGANISM: Synechococcus sp.
 415 <400> SEQUENCE: 4

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418	tggggccggg	gcagtgtgct	ccatcgttt	gtgggctggg	gacagaggtt	gatacaggct	120										
420	agtgtgctc	ggccccactt	cgaggcattt	ggtaacggctc	tagtggcaat	aatttttatt	180										
422	gcggctccct	tcacacctcc	caccatgtt	ggcattttta	tgctgctctg	tggagccttt	240										
424	tgggctctgc	tgaccttgc	tgatcaacca	gggaagggtt	tgactcccat	ccatgtttta	300										
426	gttttgcct	actggtgcat	ttcggcgatc	gccgtggat	tttctccgtt	aaaaatggcg	360										
428	gcggcgtcgg	ggttagcga	attaacagct	aatttatgtc	tgtttctact	ggggcgagg	420										
430	ttattgcaaa	acaaaacaatg	gttgaacccg	ttagtaaccg	ttgttttact	gttagggcta	480										
432	ttggtgggga	gttacggct	gwgacaacag	gtggacgggg	tagaacagtt	agccacttgg	540										
434	aatgacccca	cctctacctt	ggcccaggcc	actagggtat	atagctttt	agtaatccc	600										
436	aatctcttgg	cggcttacct	ggtgcccatg	acgggtttga	gctttagtgc	cctgggtggta	660										
438	tggcgacgg	ggtggcccaa	actgctggga	gcaaccatgg	tgattgtta	cctactctgt	720										
440	ctcttttta	cccagagccg	ggccgttgg	ctagcagtgc	tggccctggg	agctaccttc	780										
442	ctggccctt	gttacttctg	gtggttaccc	caattacc	aattttggca	acgtggct	840										
444	ttgcccctgg	cgatcgccgt	ggcgggtata	ttaggtgggg	gagcgtttagt	tgcgggtggaa	900										
446	ccgattcgac	tcagggccat	gagcattttt	gctggggcggg	aagacagcag	taataatttc	960										
448	cgcataatg	tttgggaagg	ggtaaaagcc	atgatccag	ccgccttat	cattggcatt	1020										
450	ggcccaggta	acgaagcctt	taaccaaatt	tatcctact	atatgcggcc	ccgcttcacc	1080										
452	gccctgagtg	cctattccat	ttacctagaa	attttggtg	aaacgggtgt	agttggttt	1140										
454	acctgtatgc	tctggctgtt	ggccgttacc	ctaggcaag	gcgtagaact	ggttaaacgc	1200										
456	tgtcgccaaa	ccctcgcccc	ggaaggcatc	tggattatgg	gggctttagc	ggcgatcatc	1260										
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478	1																15
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482																	30
485	Trp	Gly	Gln	Ser	Trp	Ile	Gln	Ala	Ser	Val	Leu	Trp	Pro	His	Phe	Glu	
486																	45
489	Ala	Leu	Gly	Thr	Ala	Leu	Val	Ala	Ile	Ile	Phe	Ile	Ala	Ala	Pro	Phe	
490																	60
493	Thr	Ser	Thr	Thr	Met	Leu	Gly	Ile	Phe	Met	Leu	Leu	Cys	Gly	Ala	Phe	
494	65																80
497	Trp	Ala	Leu	Leu	Thr	Phe	Ala	Asp	Gln	Pro	Gly	Lys	Gly	Leu	Thr	Pro	
498																	95
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VERIFICATION SUMMARY
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L:27 M:270 C: Current Application Number differs, Replaced Current Application No
L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date